

R. Mitra

Re-run

#6
6/25/02

RAW SEQUENCE LISTING

DATE: 06/25/2002

PATENT APPLICATION: US/09/935,390A

TIME: 10:24:44

Input Set : N:\paola\US09935390A.RAW

Output Set: N:\CRF3\06252002\I935390A.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:
 2 (i) APPLICANT: Escobedo, Jaime
 3 Quianjin, Hu
 4 Garcia, Pablo
 5 Williams, Lewis T.
 6 Kothakota, Srinivas
 7 (ii) TITLE OF INVENTION: Secreted Human Proteins
 8 (iii) NUMBER OF SEQUENCES: 38
 9 (iv) CORRESPONDENCE ADDRESS:
 10 (A) ADDRESSEE: Chiron Corporation
 11 (B) STREET: 4560 Horton Street
 12 (C) CITY: Emeryville
 13 (D) STATE: CA
 14 (E) COUNTRY: USA
 15 (F) ZIP: 94608-2916
 16 (v) COMPUTER READABLE FORM:
 17 (A) MEDIUM TYPE: Diskette
 18 (B) COMPUTER: IBM Compatible
 19 (C) OPERATING SYSTEM: DOS
 20 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 21 (vi) CURRENT APPLICATION DATA:
 C--> 22 (A) APPLICATION NUMBER: US/09/935,390A
 C--> 23 (B) FILING DATE: 22-Aug-2001
 24 (C) CLASSIFICATION:
 25 (vii) PRIOR APPLICATION DATA:
 26 (A) APPLICATION NUMBER: 08/988,671
 27 (B) FILING DATE: 1997-12-11
 28 (viii) ATTORNEY/AGENT INFORMATION:
 29 (A) NAME: Jane E. R. Potter
 30 (B) REGISTRATION NUMBER: 33,332
 31 (C) REFERENCE/DOCKET NUMBER: 1369.002
 32 (ix) TELECOMMUNICATION INFORMATION:
 33 (A) TELEPHONE: (510) 923-2718
 34 (B) TELEFAX: (510) 655-3542
 35 (C) TELEX:
 36 (2) INFORMATION FOR SEQ ID NO: 1:
 37 (i) SEQUENCE CHARACTERISTICS:
 38 (A) LENGTH: 2063 base pairs
 39 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 41 (D) TOPOLOGY: linear
 42 (ix) FEATURE:

ENTERED

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43 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
44 GAATTCGGCA CGAGGCCTCA GTCTTCCAGG GCGGCGGTGG GTGTCCGCTT CTCTCTGCTC 60
45 TTCGACTGCA CCGCACTCGC GCGTGACCCT GACTCCCCCT AGTCAGCTCA GCGGTGCTGC 120
46 CATGGCGTGG CGGCGGCGCG AAGCCGCGCT CGGGGCTCGC GGCGTGTGG CTCTGGCGTT 180
47 GCTCGCCCTG GCCCTGTGCG TGCCCGGGGC CCGGGGCCGG GCTCTCGAGT GGTTCTCGGC 240
48 CGTGGTAAAC ATCAGTACG TGGACCCGCA GACCAACCTG ACGGTGTGGA GCGTCTCGGA 300
49 GAGTGGCCGC TTCGGCGACA GCTCGCCCAA GGAGGGCGCG CATGGCCTGG TGGGCGTCCC 360
50 GTGGGCGCCC GCGGAGACC TCGAGGGCTG CGCGCCGAC ACGCGCTTCT TCGTGCCCGA 420
51 GCGGCGCGCG CGAGGGGCGG CGCCTGGGT CGCCTGGTG GCTCGTGGGG GCTGCACCTT 480
52 CAAGGACAAG GTGCTGGTGG CGGCGCGGAG GAACGCTCG GCCGTCTCC TCTACAATGA 540
53 GGAGCGCTAC GGGAACATCA CCTTGCCCAT GTCTACGCG GGAACAGGAA ATATAGTGGT 600
54 CATTATGATT AGCTATCCAA AAGGAAGAGA AATTTTGGAG CTGGTGCAAA AAGGAATTCC 660
55 AGTAACGATG ACCATAGGGG TTGGCACCAG GCATGTACAG GAGTTCATCA GCGGTCAGTC 720
56 TGTGGTGTGT TGCGCCATTG CCTTCATCAC CATGATGATT ATCTCGTTAG CTGGCTAAT 780
57 ATTTTACTAT ATACAGCGTT TCCTATATAC TGCTCTCAG ATTGGAAGTC AGAGCCATAG 840
58 AAAAGAACT AAGAAAGTTA TTGGCCAGCT TCTACTTCAT ACTGTAAAGC ATGGAGAAAA 900
59 GGGAATTGAT GTTGATGCTG AAAATTGTGC AGTGTGTATT GAAAATTTC AAGTAAAGGA 960
60 TATTATTAGA ATTCTGCCAT GCAAGCATAT TTTTCATAGA ATATGCATTG ACCCATGGCT 1020
61 TTTGGATCAC CGAACATGTC CAATGTGTAA ACTTGATGTC ATCAAAGCCC TAGGATATTG 1080
62 GGGAGAGCCT GGGGATGTAC AGGAGATGCC TGTCCCAGAA TCTCCTCCTG GAAGGGATCC 1140
63 AGCTGCAAT TTGAGTCTAG CTTTACCAGA TGATGACGGA AGTGATGACA GCAGTCCACC 1200
64 ATCAGCCTCC CCTGCTGAAT CTGAGCCACA GTGTGATCCC AGCTTTAAAG GAGATGCAGG 1260
65 AGAAAATACG GCATTGCTAG AAGCCGGCAG GAGTGACTCT CGGCATGGAG GAACCATCTC 1320
66 CTAGCACACG TGCCCACTGA AGTGCCACCA ACAGAAGTTT GGCTTGAAT AAAGGACATT 1380
67 TTATTTTTTT TACTTTAGCA CATAATTTGT ATATTTGAAA ATAATGTATA TTATTTTACC 1440
68 TATTAGATTC TGATTTGATA TACAAAGGAC TAAGATATTT TCTTCTTGAA GAGACTTTTC 1500
69 GATTAGTCCT CATATATTTA TCTACTAAAA TAGAGTGTTC ACCATGAACA GTGTGTTGCT 1560
70 TCAGACTATT ACAAAGACAA CTGGGGCAGG TACTCTAATA TAAAGGACAG GTGGTGTTC 1620
71 TAAATAATTG GCTGCTATGG TTCTGTAAAA ACCAGTTAAT TCTATTTTTC AAGGTTTTTG 1680
72 GCAAAGCACA TCAATGTTAG ACTAGTTGAA GTGGAATTGT ATAATTCAAT TCGATAATTG 1740
73 ATCTCATGGG CTTTCCCTGG AGGAAAGGTT TTTTTTGTG TTTTTTTTTT AAGAACTTGA 1800
74 AACTTGTAAG CTGAGATGTC TGAGCTTTT TTGCCCATCT GTAGTGTATG TGAAGATTC 1860
75 AAAACCTGAG AGCACTTTT CTTTGTTTAG AATTATGAGA AAGGCACTAG ATGACTTTAG 1920
76 GATTTGCATT TTTCCCTTTA TTGCCTCATT TCTGTGACG CTTGTTGGG GAGGGAAATC 1980
77 TGTTTATTTT TTCCTACAAA TAAAAAGCTA AGATTCTATA TCGCAAAAAA AAAAAAATA 2040
78 AAAAAAATA TTCCTGCGGC CGC 2063
80 (2) INFORMATION FOR SEQ ID NO: 2:
81 (i) SEQUENCE CHARACTERISTICS:
82 (A) LENGTH: 1328 base pairs
83 (B) TYPE: nucleic acid
84 (C) STRANDEDNESS: single
85 (D) TOPOLOGY: linear
86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
87 GAATTCGGCA CGAGGTAGGC AAGGGATAAA AAGGCACCTA AGGCCCTTTT GCAATAAGAA 60
88 GCCAGATGGA TAAAGGAAGT GCTGGTCACC CTGGAGGTGT ACTGGTTTGG GGAAGGTCCC 120
89 CGGCCCCCAC AGCCCTCTGG GGAGCCTCAC CCTGGCTCTC CCCACTCACC TCAGCCCTCA 180
90 GGCAGCCCTT CCACAGGGCC CCTCTCTGCG CTGGACAGCT CTGCTGGTCT CCCCCTCCCC 240
91 TGGAGAAGAA CAAGGCCATG GGTGCGCCCC TGCTGCTGCC CTTGCTGCTC CTGCTGCAGC 300
92 CGCCAGCATT TCTGCAGCCT GGTGGCTCCA CAGGATCTGG TCCAAGCTAC CTTTATGGGG 360

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93      TCACTCAACC AAAACACCTC TCAGCCTCCA TGGGTGGCTC TGTGGAAATC CCCTTCTCCT      420
94      TCTATTACCC CTGGGAGTTA GCCATAGTTC CCAACGTGAG AATATCCTGG AGACGGGGCC      480
95      ACTTCCACGG GCAGTCCCTC TACAGCACAA GGCGCCTTC CATTACAAG GATTATGTGA      540
96      ACCGGCTCTT TCTGAAGTGG ACAGAGGGTC AGGAGAGCGG CTTCTCAGG ATCTCAAACC      600
97      TCGGGAAGGA GGACAGTCT GTGTATTTCT GCCGAGTCGA GCTGGACACC CGGAGATCAG      660
98      GGAGGCAGCA GTTGACGTCC ATCAAGGGGA CCAAACCTAC CATCACCCAG GCTGTCACAA      720
99      CCACCACCAC CTGGAGGCCC AGCAGCACAA CCACCATAGC CGGCCTCAGG GTCACAGAAA      780
100     GCAAAGGGCA CTCAGAATCA TGGCACCTAA GTCTGGACAC TGCCATCAGG GTTGCATTGG      840
101     CTGTCTGCTG GCTCAAAACT GTCATTTTGG GACTGCTGTG CCTCCTCCTC CTGTGGTGGG      900
102     GGAGAAGGAA AGGTAGCAGG GCGCCAAGCA GTGACTTCTG ACCAACAGAG TGTGGGGAGA      960
103     AGGGATGTGT ATTAGCCCCG GAGGACGTGA TGTGAGACCC GCTTGTGAGT CCTCCACACT      1020
104     CGTTCCTCAT TGGCAAGATA CATGGAGAGC ACCCTGAGGA CCTTTAAAAG GCAAAGCCGC      1080
105     AAGGCAGAAG GAGGCTGGGT CCTGAATCA CCGACTGGAG GAGAGTTACC TACAAGAGCC      1140
106     TTCATCCAGG AGCATCCACA CTGCAATGAT ATAGGAATGA GGTCTGAACT CCCTGAAAT      1200
107     AAACCACTGG CATTGCGGGG CTGTTTATTA TAGCAGTGCA AAGAGTTTCT TTATCTCTCC      1260
108     CAAGGATGGA AAAATACAAT TTATTTTGCT TACCATAAAA AAAAAAAAAA AAAAATTCCT      1320
109     GCGGCCGC                                     1328
111 (2) INFORMATION FOR SEQ ID NO: 3:
112     (i) SEQUENCE CHARACTERISTICS:
113         (A) LENGTH: 1689 base pairs
114         (B) TYPE: nucleic acid
115         (C) STRANDEDNESS: single
116         (D) TOPOLOGY: linear
117     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
118     GAATTCGGCA CGAGGGCAAG ATTGCATACA AAACCAATGA ACCTGTGTGG GAGGAAAAC      60
119     TCACTTTCTT CATTACAAT CCAAGCGCC AGGACCTTGA AGTTGAGGTC AGAGACGAGC      120
120     AGCACCAGTG TTCCCTGGGG AACCTGAAGG TCCCCCTCAG CCAGCTGCTC ACCAGTGAGG      180
121     ACATGACTGT GAGCCAGCGC TTCCAGCTCA GTAACTCGGG TCCAAACAGC ACCATCAAGA      240
122     TGAAGATTGC CCTGCGGGTG CTCCATCTCG AAAAGCGAGA AAGGCTCCA GACCACCAAC      300
123     ACTCAGCTCA AGTCAAACGT CCCTCTGTGT CCAAAGAGGG GAGGAAAACA TCCATCAAAT      360
124     CTCATATGTC TGGGTCTCCA GGCCCTGGTG GCAGCAACAC AGCTCCATCC ACACCAGTCA      420
125     TTGGGGGCAG TGATAAGCCT GGATAGGAAG AAAAGGCCCA GCCCCCTGAG GCCGGCCCTC      480
126     AGGGGCTGCA CGACCTGGGC AGAAGCTCCT CCAGCCTCCT GGCTCCCCA GGCCACATCT      540
127     CAGTCAAGGA GCCGACCCCC AGCATCGCCT CGGACATCTC GCTGCCCATC GCCACCCAGG      600
128     AGCTGCGGCA AAGGCTGAGG CAGCTGGAAA ACGGGACGAC CCTGGGACAG TCTCCACTGG      660
129     GGCAGATCCA GCTGACCATC CGGCACAGCT CGCAGAGAAA CAAGCTTATC GTGGTCGTGC      720
130     ATGCTGCGAG AAACCTCATT GCCTTCTCTG AAGACGGCTC TGACCCCTAT GTCCGCATGT      780
131     ATTTATTACC AGACAAGAGG CGGTCAAGAA GGAGGAAAAC ACACGTGTCA AAGAAAACAT      840
132     TAAATCCAGT GTTTGATCAA AGCTTTGATT TCAGTGTTC GTTACCAGAA GTGCAGAGGA      900
133     GAACGCTCGA CGTTGCCGTG AAGAACAGTG GCGGCTTCCT GTCCAAAGAC AAAGGGCTCC      960
134     TTGGCAAAGT ATTGGTTGCT CTGGCATCTG AAGAACTTGC CAAAGGCTGG ACCCAGTGGT      1020
135     ATGACCTCAC GGAAGATGGG ACGAGGCCTC AGGCGATGAC ATAGCCGCAG CAGGCAGGAG      1080
136     GCGTCCTCTT CAGCGTAGCT CTCCACCTCT ACCCGGAACA CACCCTCTCA CAGACGTACC      1140
137     AATGTTATTT TTATAATTTC ATGGATTTAG TTATACATAC CTTAATAGTT TTATAAAATT      1200
138     GTTGACATTT CAGGCAAATT TGGCCAATAT TATCATTGAA TTTTCTGTGT TGGATTTCTT      1260
139     CTAGGATTTT GCCAGTTCCT ACAACGTGCA GTAGGGCGGC GGTAGCTCTT GTGTCTGTGG      1320
140     ACTCTGCTCA GCTGTGTCCG TAGGAGTCGG ATGTGTCTGT GCTTTATTAT GGCCTTGTTC      1380
141     ATATATCACT GAGGTATACT ATGCCATGTA AATAGACTAT TTTTATAAAT CTTAACATGC      1440
142     TGGTTTAAAT TCAGAAGGAA ATAGATCAAG GAAATATATA TATTTCTTTC TAAACCTTAT      1500

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143      TAAATTCGTG TGACAAATAA TCATTTTCAT CTTGGCAGCA AAAAGTTCTC AGTGACCTAT 1560
144      TTTGTGGTGT TTCTTTTGA AAAGAAAAGC TGAAATATTA TTAAATGCTA GTATGTTTCT 1620
145      GCCCATTATG AAAGATGAAA TAAAGTATTC AAAATATTAA AAAAAAAAAA AAAAAATTCC 1680
146      TCGGCCCGC                                     1689

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148 (2) INFORMATION FOR SEQ ID NO: 4:

149 (i) SEQUENCE CHARACTERISTICS:

150 (A) LENGTH: 1505 base pairs

151 (B) TYPE: nucleic acid

152 (C) STRANDEDNESS: single

153 (D) TOPOLOGY: linear

154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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155      GAATTCGGCA CGAGGAGCAG ATCTGCAAGA GTTCGTTTA TGGAGGCTGC TTGGGCAACA 60
156      AGAACAACTA CCTTCGGGAA GAAGAGTGCA TTCTAGCCTG TCGGGGTGTG CAAGGTGGGC 120
157      CTTTGAGAGG CAGCTCTGGG GCTCAGGCGA CTTTCCCCCA GGGCCCCCTC ATGGAAAGGC 180
158      GCCATCCAGT GTGCTCTGGC ACCTGTGAGC CCACCCAGTT CCGCTGCAGC AATGGCTGCT 240
159      GCATCGACAG TTTCTGGAG TGTGACGACA CCCCCAACTG CCCCAGCGCC TCCGACGAGG 300
160      CTGCCTGTGA AAAATACACG AGTGGCTTTG ACGAGCTCCA GCGCATCCAT TTCCCCAGCG 360
161      ACAAGGGGCA CTGCGTGGAC CTGCCAGACA CAGGACTCTG CAAGGAGAGC ATCCCGCGCT 420
162      GGTACTACAA CCCCTTCAGC GAACACTGCG CCGCTTTTAC CTATGGTGGT TGTACGCA 480
163      ACAAGAACAA CTTTGAGGAA GAGCAGCAGT GCCTCGAGTC TTGTCGCGGC ATCTCCAAGA 540
164      AGGATGTGTT TGGCCTGAGG CGGGAAATCC CCATTCCCAG CACAGGCTCT GTGGAGATGG 600
165      CTGTCGAGT GTTCTGGTC ATCTGCATTG TGGTGGTGGT AGCCATCTTG GGTACTGCT 660
166      TCTTCAAGAA CCAGAGAAAG GACTTCCACG GACACCACA CCACCACCA CCCACCCCTG 720
167      CCAGTCCAC TGTCTCCACT ACCGAGGACA CGGAGCACCT GGTCTATAAC CACACCACGC 780
168      GGCCCCCTG AGCCTGGGTC TCACCGGCTC TCACCTGGCC CTGCTTCTG CTTGCCAAGG 840
169      CAGAGGCCTG GGCTGGGAAA AACTTTGGAA CCAGACTCTT GCCTGTTTCC CAGGCCCACT 900
170      GTGCCTCAGA GACCAGGGCT CCAGCCCCTC TTGGAGAAGT CTCAGCTAAG CTCACGTCCT 960
171      GAGAAAGCTC AAAGGTTTGG AAGGAGCAGA AAACCCCTGG GCCAGAAGTA CCAGACTAGA 1020
172      TGGACCTGCC TGCATAGGAG TTTGGAGGAA GTTGGAGTTT TGTTCCTCT GTTCAAAGCT 1080
173      GCCTGTCCCT ACCCATGGT GCTAGGAAGA GGAGTGGGGT GGTGTCAGAC CCTGGAGGCC 1140
174      CCAACCTGT CCTCCGAGC TCCTCTTCCA TGCTGTGCGC CCAGGGCTGG GAGGAAGGAC 1200
175      TTCCCTGTGT AGTTTGTGCT GTAAAGAGTT GCTTTTGT TATTAAATGC TGTGGCATGG 1260
176      GTGAAGAGGA GGGGAAGAGG CTTGTTTGGC CTCTCTATCC TCTTCTCTC TTCCCCAAG 1320
177      ATTGAGCTCT CTGCCCTTGA TCAGCCCCAC CCTGGCCTAG ACCAGCAGAC AGAGCCAGGA 1380
178      GAAGCTCAGC TGCATTCCGC AGCCCCACC CCAAGGTTT TCCAACATCA CAGCCCAGCC 1440
179      CGCCCACTGG GTAATAAAAG TGGTTTGTGG AAAAAAAAAA AAAAAAAAAA AAGTCCTGCG 1500
180      GCCGC                                     1505

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182 (2) INFORMATION FOR SEQ ID NO: 5:

183 (i) SEQUENCE CHARACTERISTICS:

184 (A) LENGTH: 2002 base pairs

185 (B) TYPE: nucleic acid

186 (C) STRANDEDNESS: single

187 (D) TOPOLOGY: linear

188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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189      GAATTCGGCA CGAGGGCCAT GGCCGGGCTA TCCCGCGGGT CCGCGCGCGC ACTGCTCGCC 60
190      GCCCTGCTGG CGTCGACGCT GTTGGCGCTG CTCGTGTCGC CCGCGCGGGG TCGCGCGGGC 120
191      CGGGACCACG GGGACTGGGA CGAGGCCTCC CGGCTGCCGC CGCTACCACC CCGCAGGAC 180
192      GCGGCGCGCG TGGCCCGCTT CGTGACGCAC GTCTCCGACT GGGGCGCTCT GGCCACCATC 240
193      TCCACGCTGG AGGCGGTGCG CGGCCGGCCC TTCGCCGACG TCCTCTCGCT CAGCGACGGG 300

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194      CCCCCGGGCG CGGGCAGCGG CGTGCCCTAT TTCTACCTGA GCCCGCTGCA GCTCTCCGTG      360
195      AGCAACCTGC AGGAGAATCC ATATGCTACA CTGACCATGA CTTTGGCACA GACCAACTTC      420
196      TGCAAGAAAC ATGGATTGGA TCCACAAAGT CCCCTTTGTG TTCACATAAT GCTGTGAGGA      480
197      ACTGTGACCA AGGTGAATGA AACAGAAATG GATATTGCAA AGCATTGCTT ATTCATTGCA      540
198      CACCCTGAGA TGAAACCTG GCCTTCCAGC CATAATTGGT TCTTTGCTAA GTTGAATATA      600
199      ACCAATATCT GGGTCCTGGA CTACTTTGGT GGACCAAAAA TCGTGACACC AGAAGAATAT      660
200      TATAATGTCA CAGTTCAGTG AAGCAGACTG TGGTGAATTT AGCAACACTT ATGAAGTTTC      720
201      TTAAAGTGGC TCATACACAC TTAAGAGGCT TAATGTTTCT CTGGAAGCG TCCCAGAATA      780
202      TTAGCCAGTT TTCTGTCACA TGCTGGTTTG TTTGCTTGCT TGTTTACTTG CTGTTTACC      840
203      AATAGAGTTG ACCTGTTATT GGATTTCTTG GAAGATGTGG TAGCTACTTT TTTCTATTT      900
204      TGAAGCCATT TTCGTAGAGA AATATCCTTC ACTATAATCA AATAAGTTT GTCCCATCAA      960
205      TTCCAAAGAT GTTTCAGTG GTGCTCTTGA AGAGGAATGA GTACCAGTTT TAAATTGCCC      1020
206      ATTGGCATTG GAAGGTAGTT GAGTATGTGT TCTTTATTCC TAGAAGCCAC TGTGCTTGGT      1080
207      AGAGTGCATC ACTCACCACA GCTGCCTCTT GAGCTGCCTG AGCCTGGTGC AAAAGGATTG      1140
208      GCCCCATTA TGGTGCTTCT GAATAAATCT TGCCAAGATA GACAAACAAT GATGAACTC      1200
209      AGATGGAGCT TCCTACTCAT GTTGATTTAT GTCTCACAAT CCTGGGTATT GTTAATTCAA      1260
210      CATAGGGTGA AACTATTTCT GATAAAGAAC TTTTGAAAAA CTTTTTATAC TCTAAAGTGA      1320
211      TACTCAGAAC AAAAGAAAGT CATAAACTC CTGAATTTAA TTTCCCCACC TAAGTCGAGA      1380
212      CAGTATTATC AAAACACATG TGCACACAGA TTATTTTTTG GCTCCAAAAC TGGATTGCAA      1440
213      AAGAAAGAGG AGAGATATTT TGTGTGTTCC TGGTATTCTT TTATAAGTAA AGTTACCCAG      1500
214      GACTGGACCA GCTTCAGCCA GGGCAAAAAT CCCCTCCCAA ACCACTCTCC ACAGCTTTTT      1560
215      AAAAAATATT CTACTCTTAA CAATTACCTA AGGTTCCCTC AAACCCCCC AACTCTTAAT      1620
216      AGCTTCTAGT GCTGCTACAA TCTAAGTCAG GTCACCAGAG GGAAGAGAAC ATGGCATTAA      1680
217      AAGAATCACA TCTCAGAAG AGAAGACACT AATATTATTA CCCATATACA TGATTTTCAA      1740
218      AGATGACATA AGATTCTCTT TAAAGAGGAA ATGTCAGGAA TCAAGCCACT GAATCCTTAA      1800
219      AGAGAAAAGT TGAATATGAG TCATTGTGTC TGAAAACCTG AAAGTGAAC TAAGTGAGAT      1860
220      CCAGCAAACA GGTTCGTGTT AAGAAAAATA ATTTATACTA AATTTAGTAA AATGGACTTC      1920
221      TTATTCAAAG CATCAATAAT TAAAAGAATT ATTTTAAAAA AAAAAAAAAA AAAAAAAAAA      1980
222      AAAAAAAAAA TCCTGCGGCC GC                                     2002
224 (2) INFORMATION FOR SEQ ID NO: 6:
225     (i) SEQUENCE CHARACTERISTICS:
226         (A) LENGTH: 1322 base pairs
227         (B) TYPE: nucleic acid
228         (C) STRANDEDNESS: single
229         (D) TOPOLOGY: linear
230     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
231     GAATTCGGCA CGAGGGCCAC GACTCTGCTG GCATTTCTTC TATAGCCACT GGAATCTGAT      60
232     CCTGATTGTC TTCCACTACT ACCAGGCCAT CACCACTCCG CCTGGGTACC CACCCAGGG      120
233     CAGGAATGAT ATCGCCACCG TCTCCATCTG TAAGAAGTGC ATTTACCCCA AGCCAGCCCG      180
234     AACACACCAC TGCAGCATCT GCAACAGGTG TGTGCTGAAG ATGGATCACC ACTGCCCTG      240
235     GCTAAACAAT TGTGTGGGCC ACTATAACCA TCGGTACTTC TTCTCTTCT GCTTTTTTCAT      300
236     GACTCTGGGC TGTGTCTACT GCAGCTATGG AAGTTGGGAC CTTTCCGGG AGGCTTATGC      360
237     TGCCATTGAG AAAATGAAAC AGCTCGACAA GAACAAACTA CAGGCGGTTG CCAACCAGAC      420
238     TTATCACCAG ACCCCACCAC CCACCTTCTC CTTTCGAGAA AGGATGACTC ACAAGAGTCT      480
239     TGTCTACCTC TGGTTCCTGT GCAGTCTGTG GGCATTGCC CTGGGTGCCC TAACTGTATG      540
240     GCATGCTGTT CTCATCAGTC GAGGTGAGAC TAGCATCGAA AGGCACATCA ACAAGAAGGA      600
241     GAGACGTCGG CTACAGGCCA AGGGCAGAGT ATTTAGGAAT CCTTACAACT ACGGCTGCTT      660
242     GGACAACTGG AAGGTATTCC TGGGTGTGGA TACAGGAAGG CACTGGCTTA CTCGGGTGCT      720
243     CTTACCTTCT ACTCACTTGC CCCATGGGAA TGAATGAGC TGGGAGCCCC CTCCCTGGGT      780

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VERIFICATION SUMMARY

DATE: 06/25/2002

PATENT APPLICATION: US/09/935,390A

TIME: 10:24:45

Input Set : N:\paola\US09935390A.RAW

Output Set: N:\CRF3\06252002\I935390A.raw

L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:43 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:737 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:784 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:831 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:866 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:903 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:938 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:1005 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
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L:1265 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:1322 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:1373 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:1418 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:1455 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37
L:1524 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38